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Title: Bacterial Diversity Among Different Melon Types Grown in Different Locations

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Only a single study has explored the microbial diversity on melon rinds, and this was focused on a single location in Mexico. In the United States, 90% of the commercial melons are currently grown in California and Arizona, yet with growing consumer demand for more types and healthier melons, other states are starting to expand melon growing operations. The goal of this study was to determine the variation in microbial diversity among different types of melons grown in various regions around the United States. Up to 36 varieties of melons were grown in fields in six states around the United States and shipped to the University of Arizona for microbiome analysis. Melon microbiome samples were collected by swabbing a section of the rinds, swabs were DNA extracted, the V3-V4 region of the 16s rRNA gene amplified with 515F-926R primers, and then sequenced on an Illumina MiSEQ. Alpha and beta diversity and the taxonomic profile of the samples were determined using the QIIME2 pipeline for analysis. Various alpha-diversity analysis all had a high statistically significant difference in bacterial diversity among different types of melons as well as different melons grown across different states. For example, taxonomic analysis showed high levels of *Leuconostocaceae* in California that was not present in other states, while Indiana and North Carolina had *Microbacteriaceae* that was higher than other states. Understanding the bacterial diversity of different melons and regions can identify potential antagonistic and synergistic bacteria against foodborne pathogens like *Listeria* or *Salmonella* in the fields or identify variation in spoilage bacterial counts or diversity among different melon varieties or growing regions. This study lays the foundation for future research on melon varieties and their growing regions that contribute to areas of food safety, improve melon shelf-life, and could assist in improving overall melon/plant health.